

FIGURE 1

CGGACGGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCAGGGCTGCTAGGCCTC
TGTGCCCGGGCTTGGATT CGGTGCGGATGCCAGCTCCGGATGACCCGCCGGACCCGCT
CGCAAATAAGGTGCCCTGGTAACGCCCTCACCGACGGGATCGGCTCGCCATGCCCGGC
GTTTGGCCCAGGACGGGCCCCATGTGGTCGT CAGCAGCCGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGAGGGGCTGAGCGTACGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCCTTCTTGGAAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAACGAGGAGGCAGCTCAGTGGTGTCTTCCATAGCAGCCTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTGCTGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGC GGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTCCGTGCTCT
GAAGATGCCAGCTACATCACTGGGAAACAGTGGTGGTGGTGGAGGAACCCGTCGGCCT
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGCTCTAGCTCCTGGTGTGCTGTC
ATT CACCCACTGGCTTCCCACCTCTGCTCACCTACTGTTCACCTCATCAAATCAGTTCT
GCCCTGTAAAAGATCCAGCCTCCCTGCCGTCAAGGTGGCGTCTACTCGGGATTCCCTGCT
GTTGTTGTGGCCTGGGTAAAGGCCTCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTCTGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAACGGAACCTGGAGTGGAGGAGCAGAGTTGCAAATTAAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGTTGAAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T) : 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVATLQGEGLSVTGTCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGGSVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETRLIRRGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GC~~G~~CCCTGAGCTCCGCC~~T~~CCGGGCCGATAGCGCATCGAGAGCGCCTCCGTGAGGACCAGGCCGG
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCTGAGAACCAAGGTGG
GCGGCTGGAGGAGGAACCGAGACTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAAACTGC
AGAGCAGCCGGCTGCGTGAGCAGCAGGAGAGATGGTGGAACTGCGGCTGCGTTAGAGCTGGTGC
CCAGGCTGGGGGGCCTGCGCTCTGAATGGCCTGCCCTCCGGTCTTGTGCCCTGACCTCATAC
AGCCCCCCTGGGGGTGCCCACGCCATGTGCTGGCATGGTGCCTGCCCTGCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGCC
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCACTGAGTCAGAGGGGGGGCACGCC
GGAGTCTGCCAGAGAGGAAGGCCAGAGCTTGCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCAGGTTCAAGGCCAGGTCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCCAGGCCAGCAGAAAGATCCGGAGCTGGCTATCAACATCCGATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACGCCAGCACAGCAGCGTATCCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCAGCTGAGTGAAGGCCAGAGGAGCTGCC
CGAGGGCAAGGAGCTCAGGATGCTGGCGAGCGGTCTGGCTCCAGGAGTTCCGCAGGAGGGTC
CGGCCAGAGCCAGGTGCAAGGTGCTGAAGGAGAAAGCAGGCTACGGAGCGGCTGGTCACTGTC
GCCAGAGT~~G~~AGAAGCAGACTGCAAGGAGCTGAGCAGGAGCAGAAAGGCCCTGGAGGAGAAATGACA
GCTGCAAGAGGCCCTCGCGAGGAGACGGAGCAGAAAGGCCCTGGAGGAGAAATGACAAGCGGC
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAAGATCCTGAAGGATTAAGACGGAA
GAGATCGCGGCC~~T~~CCAGAGGAAGAGGCCAGTGGCAGCAACGCCCTGTGGTCAAGCCTGGAAACAGCA
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCC
CGCTGGAGGAGCTGGGGAGGAGCTCCAAGGCCATCCTGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGCTGGAGAGCAAGGCCCTGAGATCCAGGCCAGGCCCTCAACGAGGACATCGTGC
AGTGTCCAGGCCCTGGAGCACCTGGAGAAGGAGCTGTCCAGAGAGCTGCCATTGAGTATAAGAATGAGGCC
GCCAGGCCAGAGCCAGCAGATCCGCCGGAGATCGACAGCCTGCCAGGAGAAGGACTCGCTGCTC
AAGCAGGCCCTGGAGATCGACGGCAAGCTGAGGCAGGGAGTCTGCTGTCCCCCAGGAGGAGCGGC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCC
CATGCCGCCAGCGGGTCTCGGCCCTCAGCCTCGTTGCTGTCCCAGTGCAGATGAACCTCATGGCC
AAGCTCAGCTACCTCATCCTCAGAGACCAGAGGCCCTCCTGCAAGTATTTGACAAGGTGGTGA
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCCTCGGAACGGAGATGCAAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGGCCCTGGAGATGGACCAGCTGACC
CTGCAGCAGAAGGAGCAGCAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCAGAGACCACCTCGGTGA
AGGGTTAGCAGACAGCAGGAGGAGTATGAGGCCGGATTCAAGCTCTGGAGAAGGAACTGGGCC
ACATGTGGATAAAACCAGGAAC~~T~~GAAACAGAAGCTCGCGGTGTGAACCGCTGTAGGCCACAGCAGGG
GGGGAGAAGAGGAGCCTGTGCTCGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTTCTCTGGCTGCCCTCACTGAGGGGCCCGCACCCGGAGGAGACGCCGGACT
TGGTCCACGCTCCGTTACCCCTGACCTGGAAACGCTCGAGCCTGTGAGGAGCAGGGTCCCC
GAGGAAGT~~G~~AGGCAGCGGGAGGCCGAGGCCCTGGTGGGGCGGGTCTCCTGTGGTGGAGCAGG
CCTGCCCTGGAAC~~T~~TTGGCCTTGTCCAAGGCCGGGAAC~~T~~GCAGCAGGCCAGGCCGGGATGA
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GCTGAAAGGGCAGCTGCCCTGTTGCTTGTGAAGGGCAGTCCTTACCGCACACCC~~T~~AAATCCAGG
CCCTCATCTGTACCCCTACTGGGATCAACAAATTGGCCATGGCCAAAAGAACTGGACCC~~T~~CATT
AACAAAATAATATGCAAATTCCCACCACTTACTCCATGAAGCTGTGGTACCCATTGCCCTGTG
TCTTGCTCGAATCTCAGGACAATTCTGGTTCAAGCGTAAATGGATGTGCTTAGTTCAAGGG
GCCAAGAATCATCAGAAAGGGCGGTGGCAACCAGGTTGTGGTTAAATGGTCTTATGTATAGGG
GAAACTGGGAGACTT~~A~~GGATCTTAA~~A~~ACCATTAA~~A~~AAAATCTTGAAGGGAC

FIGURE 4

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465
<subunit 1 of 1, 830 aa, 1 stop
<MW: 95029, pI: 8.26, NX(S/T): 2
MEQYKLQSRTLREQQEEMVELRLRLELVRPGWGLRLLNGLPPGSFVPRPHTAPLGGAHAV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCQRAGARPGSLPERKGPELCLEELDAAPIGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAIRNIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRRLREETEQKRRLEAEMSQRQHVKELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKLQRGSLLSPEEERTLFQLDEAIEALDAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMALKSYLSSSETRALLCKYFDKVVTLREEHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLQQSRDHGLEGLADSRRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGRGKRSCLCSEGRCAPGNEDELHLAPELLWLSPTEG
APRTREETERDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL
```

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTGGAAAGCATGAGGCCACGATGCTGCATCTGGCTCTGTCTGCT
GGATAACAGTCTCCTCCTCCAGTGTCAAAGGAACACTACAGACGCTCCTGGCTCAGGA
CTGTGGCTGTGCCAGCGACACCCAGGTGTGGAACAAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTAAAGGAGACCCGCCGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTGAGCTCTGCTGTCCCAGTCTTGGCCCCAGCAGAAGTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCATCTCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACCTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGGAGAGGGAGCCAGCTGGGATGGC
CAGACTTCAGGGAAAGAATGCCTCCTGCTTCATCCCCTTCCAGCTCCCTCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCCACATTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLQLQCSKGTTDAPVGSGLWLQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCACCGCGTCCGCCACCGCTCCGGTGCCACTCGCGCGCCGCGCTCCGGCTTCTCT
TTTCCCTCCGACCGGCCACGGCTGCCAGACATTCCGGCTGCCGGTCTGGAGAGCTCCCCG
AACCCCTCCGCGAGAGGAGCGAGGGCGCCAGGGTGGCCCCGGGGCGCGCTTGGTCTCG
GAGAAGCGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGACTGACGCGAGTT
GGGGCGCGACTACCAGCTGACAGCGCATGAGCGACTCCCCAGAGACGCCCTAGCCG
GTGTGCGGCCAGGCAGCGCAGGTGGGCTGGCTTAGTGGTCCGCCAACGCGGG
TCGCCGGCCGGCCCAGGATGGCGCTGGCAACCCGGGCCGCCGCGCTGCTACCCCTG
CGCCCGCTGCGAGCCGGCGTCCGGCCGCCCTGCGCTATGGACGGCGCTCCGGCTG
GGGGCGGCCGCCGGCTGTGAATGCGACTGCCCTGGCCGCGCTCCCCGCCGCC
GCCCGCCGGACGTGGTAGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATTGGAG
AAGCTGGCCAGGCACCAGAGCAGCCGGCCAGGAGAAGCGTGAGCACGCCACTGGGACGG
CCCGGGGGGGTGAACGAGCTGGCGCCGGCGAGGGACGAGGGCGGAGCGGGCGGGACT
GGAAGAGCAAGAGCGGCCGTGGCTGCCGGCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCCAGGGGGGGCGCCAAGGCCGGGATCTGCAGGTCCGGCCCCCGGGGACAC
CCCGCAGGCCAGCCGGAGGAGTACGTGTACCGGACTACCGTGGCAAGGGCTGCGTGGAG
AGCGGCTCGTGTACGCGATCGGGAGAAGTTCGCCGGCCCTGCCGTGCCGTGCCT
GTGCACCGAGGGGGCCGCTGTGCGCGCAGCCGAGTGCCGAGGCTGCACCCGCGCTGCA
TCCACGTCGACACGAGCCAGTGCTGCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTT
CGGGGCAAGACCTATCAGACTTGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTCAAGCGTGTCCCCAGACGGAGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGCTCCCCTGCAAAAATGGTCAAACACTGCTTGAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTCCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA
CATTCTAGATGACTCTGGAACTATCAGTCAAAGAACAGACTTTGATGAGGAATAATGGAAA
TTGTTGGTACTTTCTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTC
AAAACATCAACAAGAACCTTGGCATAAAATCCTCTAAATAATGTGCTATTTCACAG
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTCATAATCCCTCATTAGAGAG
CTTATATAAGTGTGTTCTATAGATGCAGATTTAGCTGTGTTGTCAACCGTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKRHATRDGPGRVNEL
GRPARDEGGSGRDWKSKGRLLAGREPWSKLKQAWVSQGGAKAGDLQVRPRGDTPQAEALA
AAAQDAIGPELAPTPEPPEYVYPDYRGKGCVDESGFVYAIIGEKFAPGPSACPCLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNFAETAVIPAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGTATTACTGCTGCCCTCTGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTGGACAGTCAGCATGTGTGGAAGGTGTCC
GACCTACCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCAAGTGAGCCTGGTGCCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGATGGGCCCGGCCTCCCTGATC
TCCTACACCTCGTGTGCCGCCAGGAGGACTCTGCAACAACCTCGTTA**ACTCCCTCCGCT**
TTGGGCCACAGCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGCTTGTATGG
AAGGCTGTCTGGAGGGACAACAGAAAGAGATCTGCCCAAGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGACACAGGAAATTGGGCCGTGGTATGACTGAGA
ACTGCAATAGGAAAGATTCTGACCTGTCATCGGGGACCACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
GTGTCAGGAGACGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGACAAAAG
GCTGCAGCACTGTTGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
GTGCTTGTGGCCTCCTACCCACTTCTGCTCCTGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGT
CTACCTGTGTGCAGCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGCTGTCCACCAAATCG
GAGCATTCAAGGGCTGCGTGGCCAACCTCAGCTTCTGTTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
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CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCAATCTACTCACCTAACAGCA
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GCTGCATGTATCTGATAATAACAGACCCCTGTCTTTCA

FIGURE 10

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ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTCYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEJGPVGMTECNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACG**ATG**CTACGCGGCCGGCTGCCTCCTCCGGACCTCCGTAGCGCTGCCGCCGCTG
GCTGCGGCCGCTGCTCGTCTCGCTTGCGCGCTGCTCTCTTAGAGCCGAGGGACC CGGTGGC
CTCGTCGCTCAGCCCCTATT CGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGTAT
TGT CGGGCCCCGAGGCTCCGTGGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGTG
CAGCTGGTCGCCCTCATTGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGCCGCGGGTCCAGGGATGGCGGGCTAGTAGTACCG
GCAGCCGGGACCTGGGTGCGAGCCTGGCGACTGGCTTGTGGTACGCGGACTGGATGGAC
GGCAGCTAGTAGAGAAGGGACGGCAGGATATGCAGCTGGCGCTGCGTCTGGCTCGCT
CTTCCCGGCCCTTTCAGCGT GAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCCTCCTGCAGGGCTGTGGCAGCAGTACCAACCCCTGGC
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TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTGGTGTGATGTTTGACATAGATG
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTGTT CAGGATATCTTCAGCACTTGGAACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCATTCTCTCCAGTCATCCTCCAGTTGGTCATG
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CTCGAACCTGATATT GTGCTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACATTCC
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TTTATGAAGATCTGAAGAACCACTACAAGGACATCCTCAGAGTTGTCAAACCACTGAAAGA
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FIGURE 12

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RDLGAALADWPLWYADWMGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNLDLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL
```

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCCCGCGCTGCCGTGGCCCCCTAGCAACCCCTGACATGGCGCTGAGGC GGCCACCGCGAC
TCCGGCTCTCGCCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTCAAGGGGCTGCCTGATAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGCACTCATTACGGATT CGC
AGACAAGT GACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGGGCTCGTGCAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGGCCCTTATCGCTGTGAGGTCTGCTCGAAATGACCGAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTTCGCAATTCTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGGAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGTTCTGGTGTGCTTGTACTGCCCTGA
TCACGTTGGCATCTGCTGTGCATACAGACGGTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAATCAGACGGTACTACATCCGCACTGACGAGGAGGGCAGTCAGACACAAGTCATCGTTG
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GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTCGTTGGCAAAGTGTGACCA
CTACTCTTCTTACTCTAACAGCACATGAATAGAAGAATTTCCTCAAGATGGACCCGTAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGGTTCTTAATCTGTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACAGCCGTGCTGGCCCTGTGAAGCCAGCATGTTCAACCAGTGGCGTT
CAGCAGGCCACGACAGCACCATGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAACCCA
GAAAAGGCTCTTACACAGCAGCCTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCACTGAGTTGGAGAAGCTTTGGATCAGCATTGTAAGGAAACCAAAATCAGGAAG
GTAAATTGGTTGCTGAAAGAGGATCTGCTGAGGAACCCCTGCTTGTCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGCTTAAAGGCTAACGACTGAAATGGTACTGAAATATGCTTTCTATGGGCTTGTGTTATTATAAAATT
TACATCTAAATTGGCTAACGACTGAAATGGTACTGAAATATGCTTTCTATGGGCTTGTGTTATTATAAAATT
CATACAATGTTAAATAACCTATTGGCTAACGACTGAAATATGCTTTCTATGGGCTTGTGTTATTATAAAATT
TGGAAAATATCAATAATTAGAGTATTGACCCAGGAATCCTCTCATGGAAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTACACAGCAGCCTTCAAGGGAACTCATACTGCTACACATCAGACCATAGTTGCTTAGGAAACCTT
AAAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCACTCTTCAAAAGAACCTCTCAGGTTAGCTTGAAC
GCCTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACCCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGGTGCAGGCCAGGCCAGGCCAGCTAGCTACTGTTGCCCTCGCTGCCAGGAGGCCCT
GCCATCCTGGCCCTGGCAGTGGCTGCTCCAGTGAGCTTACTCACGTTGCCCTGCTTCATCCAGCACAGC
TCTCAGGTGGCACTGCAAGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTGGCTCTGTAAAGACACCTCT
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGGGTTTAAGTTGTTATTATTGTT
AAGATTGCTAACGGCAAAGGCAATTGCAAGTCTGTCAAGTACAATAACATTGTTAAAAGAAAATGGAT
CCCAGTGTCCCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTCAAACAAACCATGAT
GGAGTGGGGCCAGTCCAGCCTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAACGCTCTGAATCAAAGCAGTTTCTAATTGACTTTAAATTGGCTTACCCGCGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGACTCAGGACTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTTGCTGCCGA
GAATGGCTCACTACTCACCTTGCTTCAAGCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
AATTGCAACATGAGACTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCAGGCCCTGGCAGAGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTCTGCTGCATGGCATTCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTGGGATTCAAGCTCCAGCCTCCT
CTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCTCTTACCCCTAAACCTCTACACTAGTGC
TGGGAAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTGAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLCARLPDFLFLFRGCLIGAVNLKSSNRTPVVQEFESELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAAGGTCTTCCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCATGCCATGGTG
ATCCTGCTGACGCTGGGCCGCTCGAGCGACGACAGCGAGTTCCAGGCCTGCTGGACATCTGGTTCCGGAG
GAGAAGCCACTGCCACCCTGCTGGACACATCGGAGGAGGCCTGCTGGACATCTGGTTCCGGAG
CGCATGATCCGTTCTGAGGTCTCCGCCCTGGTGGACGCCCTGCTGGAGGCCAGCAGCTGCTGCTG
TTCGTGAGTCGTTGGCATCCCGTGTCCAGCATGAGCAAACACTCCTCAGTCCAGTGGACCCAGGAGCTGGCCAC
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCACCTGGTGGAGGTCCAGCATGAGCGC
GGCGCCTCCGGAGGCCAGACTTCCACTCCTGCTCACAGCCTCCCTGCCGCCGCCAGACAGCACAGAGGCA
CCCAAACCAAAGAGCAGCCCAGAGCAGGCCATAGGCCAGGGCGATTGGGGACCCAGCTCCGGGTGCTG
GGCCCTGAGGACGACCTGGCTGGCATGTTCCAGATTTCCCGTCAAGCCCGACCTCGGTGGCAGAGCTCC
AGTCCCCGCCCCGTCGGCCCTGCCCTGAGCAGGCCCTGGGCAGGAGCTGGCCCGTGTCCAGGGAGCCCC
GAGGTGCCGGCATCAGGTGCGTGTCCCTGAGGCCCTGCCACCTGCTCAGCTCCCCACACGGCGGTGCCCTG
GTGATGTCCATGCACCGTAGCCACTTCCGGCTGCCGCTGCGCCAGCTCTGCCAGTACAGCGCTGTG
CCACAGGACACCGGCTTCTCCTCGCTTCTCGTAAGGTGCTCCTGAGATGCTGAGTGGCTGGACAGCCCTGG
GTGGAGGGCGGGCCCTGCGGGCACAGCTCAGGATGCTGCCAGGCCCTAGCCGGCGCAGGCTCAGTGT
GTGGAGGGGGCTCCCTGCCCTGGCCAGGCCCTGGCCTCCGTAGGACCTGGAGGTGGTAGCTCCACCGTC
CGTCCGTACGCCACCTGAGGTCTGGGAGCAGTGCAGCGTGGAGGCCAGTGTACGCAAAGTCCCTCAG
GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTCTGCCACTGCCAGTGTGCC
TCCCCGTTCCAGCCTGTAAGCCGTTGGTAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGG
GGGAAGCGGGTGGGACGGTGGCAGCTGGAGGCCGTGGCTGGGGCCCTGTCAGGCCCTCTAGGGACTGG
CTGGAAATGCTGGACCCGAGGTGGTCAGCAGCTGCCCGACCTGCACTCAGGCTGCTCTTCTCCGGAGGAAG
GGCAAAGGTCAAGGCCAGGTGCCCTGTTCCGTCACCTCCTGACCCCTTCAACGCTCAGGCCAGTGGCC
ACACTGCACCAAGTGCATCCGAGTCTGCTGGCAAGAGCCGGAACAGAGGTTGACCCCTGCTCTGAC
TTCCCTGGGCTGCATCCATGTTCTGCATCTGGCAGGGGGGGGACAGCGCACCCCGCAGAACGGGGGGAG
GAGCTGGTGTGGGGTCCAGGGCCGGAGCTCATCAGCCTGGTAGCTGATCTGGCCGAGGGAGACCGCG
AGCCAGGACGGGACACAGCCGCTGCAAGCTCATCCAGGCCGGCTGCCCTGCTGCTCAGCTGCTGTTGG
GACGATGAGAGTGTCAAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGAGACAGCGTGTGG
AGGCCTGCCAGACCTTCTCTGCAGCTCACCTACAGCGGGGAGCTGGGGTGGCCGTGCTGAGGTCTTA
CTGCACAGCGAAGGGCTGCCAGCAGCGCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
GCGGACACCAGCAGCTCCGGCGTTGGAGAACCGAGGGGGGGATGCCAGCATGGCCTGCCGAAGCTGGGGGTG
GCGCACCCGCTGCTGCTCAGGACACTGCCATGATGCCGGCTCTGCCAGGGGCCACCCACCTCAACTTC
CAGGAGTTCCGGCAGCAGAACACCACCTGAGCTGCTCTGCCAGCTGCTGGAGCTGCTGAGCGCCGAC
GTGTTCCGCAAGCGAGCACAGGGGGCGTGTGGGACTGCCTTCTGTCTTCACTCCGCTGCTGCTGAATTACAGG
AAGTCCTCCGCCATCTGGCTGCCATCAACAAGTTGTCAAGTTCATCCATAAGTACATTACCTACAATGCC
CCAGCAGCCATCTCTTCTGCAGAACAGCACGCCGACCGCTCCAGCACCTGCTCTGACAAACAGTGA
CTGGTGAGCTGGGGCTCAGCCTGCCAGCAGGGAGCACAGGACCGAGGCCCTGGACGAAGAG
GGCAGGGAGGAGAGCTCAGCCGGCTCTGGTCAAGCTGCCCTGTTCAACCCCTCTGACCGCGGGCGAG
ATGGCCCCCTACATGAAACGGCTTCCGGGCAAACGGTGGAGGATGCTGGAGGTTCTGAGTGA
GAGATGCTCCGGGGAGACCCGAGATCCTGAGCTTCTCTGCCACCAACCTGCA
GAGCTGGGGCTGAGCTGGGGCTCAGCCTGCCAGCAGGGAGCACAGGACCGAGGCCCTGGACGAAGAG
GAGTGTGGCAACCTCGCTTCACTGCCAGCAGGGCTCAGCCTGCCAGCAGGGAGCACAGGACCGAGGCCCTGGACGAAGAG
CTGCCACGTTCACTGACTGCCAGGACTTTGAGGTGGTCAAGACGCCCTGCCAGGCCCTGGACGAAGAG
TACGCTCTCTGTCAGGCCAAGAGCACGCCAGGAGGAGGATGCTGCCACCGGGCTTCTGGTGGCATG
GACCCCCAGCGCAGATCTCGAGGCCCTGAGGATCTGCATATGGAGGCCGTGATGAGCTGGGGAG
CCCCCTCCAAGGCCCGGCCGTCCTGGGGATCCTCGAGGCCAGGCAAAGGCCAGGAAGCGTGGGGCTTGTGG
TCTGTCCAGGGAGGTGAGGGGCCAGGCCCTGAGGCCAGGAGGCCAGGAGCAATACTCGAGGCCCTGGGGTGG
CTCCGGGCCGGCCGCTGGCATCAGGGGCCGTCAGCAAGGCCCTATTCAACCTCTGGGCCACAGGCCCTGCCCGCG
AGCGGGGAGATCCCCCGGGCATGGCTGGGCTGGTTTGAATGAAACGACCTGA
ACTGTCAA

FIGURE 16

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631
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><subunit 1 of 1, 1029 aa, 1 stop
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><MW: 114213, pI: 6.42, NX(S/T): 0
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MHILVVHAMVILLTGPPRADDSEFQALLDIWFPPEEKPLPTAFLVDTSEEALLLPDWLKLRM  
IRSEVLRVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRDSTEAPPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMHRSHFLACPLLRLQCQYQRCVPQDTGFSSLFLKVLLQMLQWLDSRG  
VEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFRQDLEVSVSSTVRAVIATLRSGEQ  
CSVEPDLSISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEEPLA  
GGKPGADGGSLEAVRLGPSSGLLWDLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR  
PYLLTLFTHQSSWPTLHQCI RVLLGKSREQRFDPSASLDLWACIHVPRIWQGRDQRTPKR  
REELVLRVQGP ELISLVELLAEAEATRSQDGDTAACSLIQARLPLLLSCCGDDESVRKVTE  
HLSGCIQOWGDSVLGRRCRDLLLQLYLQRPELRVPVPEVLLHSEGAASSVCKLDGLIHRFI  
TLLADTSRALSRALENRGADASMACRKLAVAHPLLLRHPMIAALLHGRTHLFQEFRQQNHL  
SCFLHVGLLELLQPHVFRSEHQGALWDCLLSFIRLLNYRKSSRHLAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG  
SLPLVSVSLFTPPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDEMSRRRPEILSFFSTNLQRL  
MSSAEECCRNLAFSLALRSMQNSPSIAAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM
```

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTGGCCCCGGCGCCGCCGCGCACCGAGGAGATGAGGCTCCGC
AATGGCACCTCCTGACGCTGCTCTTCTGCCTGTGCGCTTCCTCGCTGTCCGGTA
CGGGCACTCAGCGGCCAGAAAGGCACGTTGAGACGTTTACCAAGCGGGAGTTCTGGCGC
TGGCGATCGGTTGACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA
TCGCACCTGGGGCCGCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGCACCTGCCACCGTCTTCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCGCGGTGCGGTGGCCAGGGCCGACCGGAGTGTGGTGGTATGGCATCCC
GAGCGTGCGGCGCGAGGTGACTCGTACACTGACACTCTGCACTCGCTCATCTCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTATCGTGGTGTGATCGCCAGACTGACTCACAG
TACACTTGGCAGTGAACAGAGAACATCAAGGCCCTGTTCCCCACGGAGATCCATTCTGGGCT
CCTGGAGGTACATCTCACCCCTCCCCCCTACCTTACCCCTGACTTCTCCGCTCCGAGAGTCCT
TTGGGGACCCCAAGGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCGCAGTCAAAGGCATCTACTACGTGCACTGGAGGATGACATCGGGCAA
GCCCAACTACCTGAGCACCATGAAGAACCTTGCACTGCACTGAGCAGCCTCAGAGGACTGGATGA
TCCTGGAGTTCTCCAGCTGGCTTATTGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCATCTCATGTTACCGGGACAAGCCCATCGACTGGCTCTGGACCATA
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCAGTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTCAAACCGTCCCTTTCCAGCACGTGGCACTCACTCCTCGCTGGCT
GGCAAGATCCAGAAACTGAAGGACAAGACTTTGAAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCGCACTTACCCCTGGAGAAAG
CCTACCTGCGCGAGGACTTCTCTGGCCTTCACCCCTGCCGCGGGGACTTCATCCGCTTC
CGCTTCTCCAACCTCTAACAGACTGGAGCGGTCTTCTCCGCACTGGAAACATCGAGCACCC
GGAGGACAAGCTTCAACACGTCTGAGGAGGTGCTGCCCTCGACAACCCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGCACGCCACCCCTCCGGTACCCCTGGAGCCCCGACGGCTAC
CTCCAGATCGGCTCTTCTACAAGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTCGGCC
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCTGTGTGGTGATTCTGAGCGAGA
TCTTCCTGAAAAAGGCCGACTAAGCTGCGGGCTCTGAGGGTACCCCTGTGGCCAGCCCTGAA
GCCACATTCTGGGGTGTGTCGTCAGCCGCTCCGGAGGGCAGATACGGCCCCGCCAA
AGGGTTCTGCCTGGCGTCGGCCTGGGCCGCGCTGGGTCCGCCGCTGGCCGGAGGCC
GGAGCTGGTGTGCCCGCCGGCCGAGGAGGCAGGCGGCCACACTGTGCC
TGAGGCCCGAACCGTTGCAACCCGGCTGCCCTCAGTCAGGCCGTTTAGAAGAGCTTTAC
TTGGCGCCCGCCGTCTGGCGCAACACTGGAATGCATATACTACTTTATGTGCTGTGTT
TTTTATTCTGGATACATTGATTTTACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAAATAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pi: 8.10, NX(S/T): 4
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ELNLVLDEIKRAVSERQALRDGDGNRTWGRITEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLLAE
TDSQYTSAVTENIKALFPTEIHSGILLEVISPSYPDFSRRESFGDPKERVRWRTKQNL
YCFLMMYAQSkgIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDQDFGKQALRKEHVNPPEAVSTSLKTYQHFTLEKAYLREDFFWAFTPAGD
FIRFRFFQPLRLERFFFSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGERVDPAGPLEALRLSIQTDSPVWVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515